



PTO/SB/08A (10-01)

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Substitute for form 1449A/PTO INFORMATION DISCLOSURE STATEMENT BY APPLICANT (use as many sheets as necessary)			Complete if Known		
			Application Number	10/047,724	
			Filing Date	January 15, 2002	
			First Named Inventor	Vince Hilser	
			Art Unit	1631 1631	
			Examiner Name	Not Yet Assigned LY	
Sheet	1	of	1	Attorney Docket Number	HO-P02070US1

U.S. PATENT DOCUMENTS					
Examiner Initials*	Cite No. ¹	Document Number	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear
		Number-Kind Code ² (if known)			
CE	AA	US-6,403,312-B1	06-11-2002	Daijyat et al.	

FOREIGN PATENT DOCUMENTS						
Examiner Initials*	Cite No. ¹	Foreign Patent Document	Publication Date MM-DD-YYYY	Name of Patentee or Applicant of Cited Document	Pages, Columns, Lines, Where Relevant Passages or Relevant Figures Appear	T ⁶
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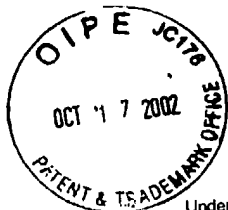
¹ Applicant's unique citation designation number (optional). ² See attached Kinds Codes of USPTO Patent Documents at www.uspto.gov or MPEP 901.04. ³ Enter Office that issued the document, by the two-letter code (WIPO Standard ST.3). ⁴ For Japanese patent documents, the indication of the year of the reign of the Emperor must precede the application number of the patent document. ⁵ Kind of document by the appropriate symbols as indicated on the document under WIPO Standard ST. 16 if possible. ⁶ Applicant is to place a check mark here if English language Translation is attached.

NON PATENT LITERATURE DOCUMENTS			
Examiner Initials*	Cite No. ¹	Include name of the author (in CAPITAL LETTERS), title of the article (when appropriate), title of the item (book, magazine, journal, serial, symposium, catalog, etc), date, page(s), volume-issue number(s), publisher, city and/or country where published.	T ²
CE	CA	Delagrave et al, "Searching Sequence Space to Engineer Proteins: Exponential Ensemble Mutagenesis," Bio/Technology Vol. 11, December 1993, pp. 1548-1552.	

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Examiner Signature		Date Considered	7/21/04
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PTO/SB/08B (10-01)

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Substitute for form 1449B/PTO		Complete if Known	
		Application Number	10/047,724
INFORMATION DISCLOSURE STATEMENT BY APPLICANT (use as many sheets as necessary)		Filing Date	January 15, 2002
		First Named Inventor	Dr. Vince Hilser
		Group Art Unit	N/A 1631
		Examiner Name	Not Yet Assigned
		Attorney Docket Number	HO-P02070US1
Sheet	3	of	4

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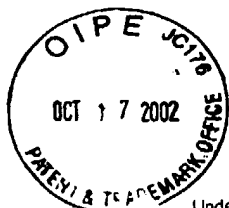
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CV	Jones, David T., et al.; FOLD RECOGNITION: PREDICTION REPORTS - Successful Recognition of Protein Folds Using Threading Methods Biased by Sequence Similarity and Predicted Secondary Structure; PROTEINS: Structure, Function, and Genetics Suppl 3:104-111 (1999)
CW	Kabsch, Wolfgang, et al.; Dictionary of Protein Secondary Structure: Pattern Recognition of Hydrogen-Bonded and Geometrical Features; Biopolymers, Vol. 22, pages 2577-2637, 1983
CX	Kuroda, Yutaka, et al.; Folding of Bovine Pancreatic Trypsin Inhibitor (BPTI) Variants in which Almost Half the Residues are Alanine; J. Mol. Biol. (2000) 298, 493-501
CY	Lee, Kon Ho, et al.; Estimation of Changes in Side Chain Configurational Entropy in Binding and Folding: General Methods and Application to Helix Formation; PROTEINS: Structure, Functional, and Genetics 20:68-84 (1994)
CZ	Llinas, Manuel, et al.; Articles: The energetics of T4 lysozyme reveal a hierarchy of conformations; nature structural biology, Vol. 6 (11), pages 1072-1078, November 1999
CA1	Murzin, Alexey G., et al.; Communication - SCOP: A structural Classification of Proteins Database for the Investigation of Sequences and Structures; J. Mol. Biol. (1995) 247, 536-540
CB1	Park, Jong, et al.; Sequence Comparisons Using Multiple Sequences Detect Three Times as Many Remote Homologues as Pairwise Methods; J. Mol. Biol. (1998) 284, 1201-1210
CC1	Arajo, Antonio F. Pereira, et al.; Thermodynamics of Interactions between Amino Acid Side Chains: Experimental Differentiation of Aromatic-Aromatic, Aromatic-Aliphatic, and Aliphatic-Aliphatic Side-Chain Interactions in Water; Biophysical Journal, Vol. 76, pages 2319 - 2328, May 1999
CD1	Pochapsky, Thomas C., et al.; A chromatographic approach to the determination of relative free energies of interaction between hydrophobic and amphiphilic amino acid side chains; Protein Science (1992), 1, 786-795
CE1	Rice, Danny W., et al.; A 3D-1D Substitution Matrix for Protein Fold Recognition that Includes Predicted Secondary Structure of the Sequence; J. Mol. Biol. (1997) 267, 1026-1038
CF1	Sadqi, Mourad, et al.; The Native State Conformational Ensemble of the SH3 Domain from a-Spectrin; Biochemistry 1999, 38, 8899-8906
CG1	Smith, T. F., et al.; Identification of Common Molecular Subsequences; J. Mol. Biol. (1981), 147, 195-197
CH1	Swint-Kruse, Liskin, et al.; Temperature and pH Dependences of Hydrogen Exchange and Global Stability for Ovomuroid Third Domain; Biochemistry 1996, 35, 171-180
CI1	Xie, Dong, et al.; Structure Based Prediction of Protein Folding Intermediates; J. Mol. Biol. (1994) 242, 62-80
CJ1	Wrabl, James O., et al.; Thermodynamic propensities of amino acids in the native state ensemble: Implications for fold recognition; Protein Science (2001), 10:1032-1045

Examiner Signature	<i>[Signature]</i>	Date Considered	7/21/04
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*EXAMINER: Initial if reference considered, whether or not citation is in conformance with MPEP 609. Draw line through citation if not in conformance and not considered. Include copy of this form with next communication to applicant.

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Substitute for form 1449B/PTO INFORMATION DISCLOSURE STATEMENT BY APPLICANT (use as many sheets as necessary)		Complete if Known	
		Application Number	10/047,724
		Filing Date	January 15, 2002
		First Named Inventor	Dr. Vince Hilser
		Group Art Unit	1631 1631
		Examiner Name	Not Yet Assigned LPT
Attorney Docket Number	HO-P02070US1		
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OTHER PRIOR ART - NON PATENT LITERATURE DOCUMENTS			
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apl	CA	Hilser, Vincent J., et al.; Structure-based Calculatin of the Equilibrium Folding Pathway of Proteins. Correlation with Hydrogen Exchange Protection Factors; J. Mol. Biol. (1996) 262, 756-772	
	CB	Gribskov, Michael, et al.; Profile analysis: Detection of distantly related proteins; Proc. Natl. Acad. Sci. USA Vol. 84, pp. 4355-4358, July 1987, Biochemistry	
	CC	Pan, Hong, et al.; Binding sites in Escherichia coli dihydrofolate reductase communicate by modulating the conformational ensemble; PNAS, Vol. 97 (22), 12020-12025, October 24, 2000	
	CD	Hilser, Vincent J., et al.; The structural distribution of cooperative interactions in proteins: Analysis of the native state ensemble. Proc. Natl. Acad. Sci. USA, Vol. 95, pp. 9903-9908, August 1998, Biophysics	
	CE	Bowie, James U., et al.; A Method to Identify Protein Sequences That Fold into a Known Three-Dimensional Structure. Science, Vol. 253, pages 164-170, July 12, 1991 (Research Article)	
	CF	Altschul, Stephen F., et al.; Gapped BLAST and PSI-BLAST: a new generation of protein database search programs. Nucleic Acids Research, 1997, Vol. 25, No. 17, pages 3389-3402	
	CG	Anfinsen, Christian B., Principles that Govern the Folding of Protein Chains; SCIENCE, Vol. 181, No. 4096, pages 223-230, July 20, 1973	
	CH	Bai, Yawen, et al.; FUTURE DIRECTIONS: Future Directions in Folding: The Multi-State Nature of Protein Structure; PROTEINS: Structure, Function, and Genetics 24:145-151(1996)	
	CI	Baker, David, et al.; A protein-folding reaction under kinetic control; Nature, Vol. 356, pages 263-265; March 19, 1992	
	CJ	Baldwin, Robert L.; Temperature dependence of the hydrophobic interaction in protein folding; proc. Natl. Acad. Sci. USA, Vol. 83, pp. 8069-8072, November 1986, Biochemistry	
	CK	Chamberlain, Aaron K., et al.; Detection of rare partially folded molecules in equilibrium with the native conformation of RNaseH; Nature Structural Biology, Vol. 3 (9), pages 782-787, September 9, 1996	
	CL	Cohen, Fred E.; Protein Misfolding and Prion Diseases; J Mol. Biol. 293:313-320, 1999	
	CM	D'Aquino, J. Alejandro, et al.; Research Articles: The Magnitude of the Backbone Conformational Entropy Change in Protein Folding; PROTEINS: Structure, Function, and Genetics 25:143-156 (1996)	
	CN	Feldman, Douglas, et al.; Protein folding in vivo: the importance of molecular chaperones; Structural Biology 2000, 10:26-33	
	CO	Fink, Anthony L.; Chaperone-Mediated Protein Folding; Physiological Reviews, Vol. 79 (2), April 1999 425-449	
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	CQ	Habermann, Susan M., et al.; Energetics of hydrogen bonding in proteins: A model compound study; Protein Science (1996), 5:1229-1239	
	CR	Hobohm, Uwe, et al.; FOR THE RECORD: Enlarged representative set of protein structures; Protein Science (1994), 3:522-524	
	CS	Huyghues-Despointes, Beatrice M. P., et al.; Hydrogen-Exchange Stabilities of RNase T1 and Variants with Buried and Solvent-Exposed Ala → Gly Mutations in the Helix; Biochemistry 1999, 38, 16481-16490	
	CT	Jackson, Sophie E.; How do small single-domain proteins fold?; Folding & Design 3:R81-R91, August 1, 1998	
	CU	Jaravine, Victor A., et al.; Microscopic stability of cold shock protein A examined by NMR native state hydrogen exchange as a function of urea and trimethylamine N-oxide; Protein Science 9:290-301, 2000	